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RAW SEQUENCE LISTING

DATE: 12/14/2001

PATENT APPLICATION: US/09/731,175

TIME: 16:07:35

Input Set : N:\Crif3\RULE60\09731175.txt

Output Set: N:\CRF3\12142001\I731175.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Glorioso, Joseph C.

7 Evans, Christopher H.

8 Robbins, Paul D.

10 (ii) TITLE OF INVENTION: Gene Transfer for Studying and Treating
11 a Connective Tissue of a Mammalian Host

13 (iii) NUMBER OF SEQUENCES: 8

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

17 (B) STREET: Two Embarcadero Center, Eighth Floor

18 (C) CITY: San Francisco

19 (D) STATE: California

20 (E) COUNTRY: USA

21 (F) ZIP: 94111-3834

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/731,175

C--> 31 (B) FILING DATE: 05-Dec-2000

32 (C) CLASSIFICATION:

58 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/924,777

36 (B) FILING DATE: 2000-01-31

39 (A) APPLICATION NUMBER: US 07/963,928

40 (B) FILING DATE: 20-OCT-1992

43 (A) APPLICATION NUMBER: US 08/027,750

44 (B) FILING DATE: 08-MAR-1993

47 (A) APPLICATION NUMBER: US 08/183,563

48 (B) FILING DATE: 18-JAN-1994

51 (A) APPLICATION NUMBER: US 08/381,603

52 (B) FILING DATE: 27-JAN-1995

55 (A) APPLICATION NUMBER: US 08/567,710

56 (B) FILING DATE: 05-DEC-1995

59 (A) APPLICATION NUMBER: US 08/685,212

60 (B) FILING DATE: 23-JUL-1996

62 (viii) ATTORNEY/AGENT INFORMATION:

63 (A) NAME: Bastian, Kevin L.

64 (B) REGISTRATION NUMBER: 34,774

65 (C) REFERENCE/DOCKET NUMBER: 018484-002280US

67 (ix) TELECOMMUNICATION INFORMATION:

68 (A) TELEPHONE: (415) 576-0200

69 (B) TELEFAX: (415) 576-0300

72 (2) INFORMATION FOR SEQ ID NO: 1:

ENTERED

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74      (i) SEQUENCE CHARACTERISTICS:
75          (A) LENGTH: 1770 base pairs
76          (B) TYPE: nucleic acid
77          (C) STRANDEDNESS: single
78          (D) TOPOLOGY: linear
80      (ii) MOLECULE TYPE: cDNA
83      (ix) FEATURE:
84          (A) NAME/KEY: CDS
85          (B) LOCATION: 55..1764
86          (D) OTHER INFORMATION: /product= "human interleukin-1 receptor"
89      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
91 CCTCCTGAGA AGCTGGACCC CTTGGTAAAA GACAAGGCCT TCTCCAAGAA GAAT ATG      57
92                                         Met
93                                         1
95 AAA GTG TTA CTC AGA CTT ATT TGT TTC ATA GCT CTA CTG ATT TCT TCT      105
96 Lys Val Leu Leu Arg Leu Ile Cys Phe Ile Ala Leu Leu Ile Ser Ser
97           5              10              15
99 CTG GAG GCT GAT AAA TGC AAG GAA CGT GAA GAA AAA ATA ATT TTA GTG      153
100 Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val
101           20              25              30
103 TCA TCT GCA AAT GAA ATT GAT GTT CGT CCC TGT CCT CTT AAC CCA AAT      201
104 Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn
105           35              40              45
107 GAA CAC AAA GGC ACT ATA ACT TGG TAT AAA GAT GAC AGC AAG ACA CCT      249
108 Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro
109           50              55              60              65
111 GTA TCT ACA GAA CAA GCC TCC AGG ATT CAT CAA CAC AAA GAG AAA CTT      297
112 Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu
113           70              75              80
115 TGG TTT GTT CCT GCT AAG GTG GAG GAT TCA GGA CAT TAC TAT TGC GTG      345
116 Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val
117           85              90              95
119 GTA AGA AAT TCA TCT TAC TGC CTC AGA ATT AAA ATA AGT GCA AAA TTT      393
120 Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe
121           100             105             110
123 GTG GAG AAT GAG CCT AAC TTA TGT TAT AAT GCA CAA GCC ATA TTT AAG      441
124 Val Glu Asn Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe Lys
125           115             120             125
127 CAG AAA CTA CCC GTT GCA GGA GAC GGA GGA CTT GTG TGC CCT TAT ATG      489
128 Gln Lys Leu Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr Met
129           130             135             140             145
131 GAG TTT TTT AAA AAT GAA AAT AAT GAG TTA CCT AAA TTA CAG TGG TAT      537
132 Glu Phe Phe Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp Tyr
133           150             155             160
135 AAG GAT TGC AAA CCT CTA CTT CTT GAC AAT ATA CAC TTT AGT GGA GTC      585
136 Lys Asp Cys Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly Val
137           165             170             175
139 AAA GAT AGG CTC ATC GTG ATG AAT GTG GCT GAA AAG CAT AGA GGG AAC      633
140 Lys Asp Arg Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly Asn

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141	180	185	190	
143	TAT ACT TGT CAT GCA TCC TAC ACA TAC TTG GGC AAG CAA TAT CCT ATT	681		
144	Tyr Thr Cys His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro Ile			
145	195 200 205			
147	ACC CGG GTA ATA GAA TTT ATT ACT CTA GAG GAA AAC AAA CCC ACA AGG	729		
148	Thr Arg Val Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr Arg			
149	210 215 220 225			
151	CCT GTG ATT GTG AGC CCA GCT AAT GAG ACA ATG GAA GTA GAC TTG GGA	777		
152	Pro Val Ile Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu Gly			
153	230 235 240			
155	TCC CAG ATA CAA TTG ATC TGT AAT GTC ACC GGC CAG TTG AGT GAC ATT	825		
156	Ser Gln Ile Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp Ile			
157	245 250 255			
159	GCT TAC TGG AAG TGG AAT GGG TCA GTA ATT GAT GAA GAT GAC CCA GTG	873		
160	Ala Tyr Trp Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro Val			
161	260 265 270			
163	CTA GGG GAA GAC TAT TAC AGT GTG GAA AAT CCT GCA AAC AAA AGA AGG	921		
164	Leu Gly Glu Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg Arg			
165	275 280 285			
167	AGT ACC CTC ATC ACA GTG CTT AAT ATA TCG GAA ATT GAA AGT AGA TTT	969		
168	Ser Thr Leu Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg Phe			
169	290 295 300 305			
171	TAT AAA CAT CCA TTT ACC TGT TTT GCC AAG AAT ACA CAT GGT ATA GAT	1017		
172	Tyr Lys His Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile Asp			
173	310 315 320			
175	GCA GCA TAT ATC CAG TTA ATA TAT CCA GTC ACT AAT TTC CAG AAG CAC	1065		
176	Ala Ala Tyr Ile Gln Leu Ile Tyr Pro Val Thr Asn Phe Gln Lys His			
177	325 330 335			
179	ATG ATT GGT ATA TGT GTC ACG TTG ACA GTC ATA ATT GTG TGT TCT GTT	1113		
180	Met Ile Gly Ile Cys Val Thr Leu Thr Val Ile Ile Val Cys Ser Val			
181	340 345 350			
183	TTC ATC TAT AAA ATC TTC AAG ATT GAC ATT GTG CTT TGG TAC AGG GAT	1161		
184	Phe Ile Tyr Lys Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg Asp			
185	355 360 365			
187	TCC TGC TAT GAT TTT CTC CCA ATA AAA GCT TCA GAT GGA AAG ACC TAT	1209		
188	Ser Cys Tyr Asp Phe Leu Pro Ile Lys Ala Ser Asp Gly Lys Thr Tyr			
189	370 375 380 385			
191	GAC GCA TAT ATA CTG TAT CCA AAG ACT GTT GGG GAA GGG TCT ACC TCT	1257		
192	Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Val Gly Glu Gly Ser Thr Ser			
193	390 395 400			
195	GAC TGT GAT ATT TTT GTG TTT AAA GTC TTG CCT GAG GTC TTG GAA AAA	1305		
196	Asp Cys Asp Ile Phe Val Phe Lys Val Leu Pro Glu Val Leu Glu Lys			
197	405 410 415			
199	CAG TGT GGA TAT AAG CTG TTC ATT TAT GGA AGG GAT GAC TAC GTT GGG	1353		
200	Gln Cys Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Asp Tyr Val Gly			
201	420 425 430			
203	GAA GAC ATT GTT GAG GTC ATT AAT GAA AAC GTA AAG AAA AGC AGA AGA	1401		
204	Glu Asp Ile Val Glu Val Ile Asn Glu Asn Val Lys Lys Ser Arg Arg			
205	435 440 445			

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207 CTG ATT ATC ATT TTA GTC AGA GAA ACA TCA GGC TTC AGC TGG CTG GGT      1449
208 Leu Ile Ile Ile Leu Val Arg Glu Thr Ser Gly Phe Ser Trp Leu Gly
209 450      455      460      465
211 GGT TCA TCT GAA GAG CAA ATA GCC ATG TAT AAT GCT CTT GTT CAG GAT      1497
212 Gly Ser Ser Glu Glu Gln Ile Ala Met Tyr Asn Ala Leu Val Gln Asp
213      470      475      480
215 GGA ATT AAA GTT GTC CTG CTT GAG CTG GAG AAA ATC CAA GAC TAT GAG      1545
216 Gly Ile Lys Val Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr Glu
217      485      490      495
219 AAA ATG CCA GAA TCG ATT AAA TTC ATT AAG CAG AAA CAT GGG GCT ATC      1593
220 Lys Met Pro Glu Ser Ile Lys Phe Ile Lys Gln Lys His Gly Ala Ile
221      500      505      510
223 CGC TGG TCA GGG GAC TTT ACA CAG GGA CCA CAG TCT GCA AAG ACA AGG      1641
224 Arg Trp Ser Gly Asp Phe Thr Gln Gly Pro Gln Ser Ala Lys Thr Arg
225      515      520      525
227 TTC TGG AAG AAT GTC AGG TAC CAC ATG CCA GTC CAG CGA CGG TCA CCT      1689
228 Phe Trp Lys Asn Val Arg Tyr His Met Pro Val Gln Arg Arg Ser Pro
229 530      535      540      545
231 TCA TCT AAA CAC CAG TTA CTG TCA CCA GCC ACT AAG GAG AAA CTG CAA      1737
232 Ser Ser Lys His Gln Leu Leu Ser Pro Ala Thr Lys Glu Lys Leu Gln
233      550      555      560
235 AGA GAG GCT CAC GTG CCT CTC GGG TAGCATGGA      1770
236 Arg Glu Ala His Val Pro Leu Gly
237      565
240 (2) INFORMATION FOR SEQ ID NO: 2:
242 (i) SEQUENCE CHARACTERISTICS:
243 (A) LENGTH: 569 amino acids
244 (B) TYPE: amino acid
245 (D) TOPOLOGY: linear
247 (ii) MOLECULE TYPE: protein
249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
251 Met Lys Val Leu Leu Arg Leu Ile Cys Phe Ile Ala Leu Leu Ile Ser
252 1      5      10      15
254 Ser Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu
255      20      25      30
257 Val Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro
258      35      40      45
260 Asn Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr
261      50      55      60
263 Pro Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys
264 65      70      75      80
266 Leu Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys
267      85      90      95
269 Val Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys
270      100      105      110
272 Phe Val Glu Asn Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe
273      115      120      125
275 Lys Gln Lys Leu Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr
276      130      135      140

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278 Met Glu Phe Phe Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp
279 145 150 155 160
281 Tyr Lys Asp Cys Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly
282 165 170 175
284 Val Lys Asp Arg Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly
285 180 185 190
287 Asn Tyr Thr Cys His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro
288 195 200 205
290 Ile Thr Arg Val Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr
291 210 215 220
293 Arg Pro Val Ile Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu
294 225 230 235 240
296 Gly Ser Gln Ile Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp
297 245 250 255
299 Ile Ala Tyr Trp Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro
300 260 265 270
302 Val Leu Gly Glu Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg
303 275 280 285
305 Arg Ser Thr Leu Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg
306 290 295 300
308 Phe Tyr Lys His Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile
309 305 310 315 320
311 Asp Ala Ala Tyr Ile Gln Leu Ile Tyr Pro Val Thr Asn Phe Gln Lys
312 325 330 335
314 His Met Ile Gly Ile Cys Val Thr Leu Thr Val Ile Ile Val Cys Ser
315 340 345 350
317 Val Phe Ile Tyr Lys Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg
318 355 360 365
320 Asp Ser Cys Tyr Asp Phe Leu Pro Ile Lys Ala Ser Asp Gly Lys Thr
321 370 375 380
323 Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Val Gly Glu Gly Ser Thr
324 385 390 395 400
326 Ser Asp Cys Asp Ile Phe Val Phe Lys Val Leu Pro Glu Val Leu Glu
327 405 410 415
329 Lys Gln Cys Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Asp Tyr Val
330 420 425 430
332 Gly Glu Asp Ile Val Glu Val Ile Asn Glu Asn Val Lys Lys Ser Arg
333 435 440 445
335 Arg Leu Ile Ile Ile Leu Val Arg Glu Thr Ser Gly Phe Ser Trp Leu
336 450 455 460
338 Gly Gly Ser Ser Glu Glu Gln Ile Ala Met Tyr Asn Ala Leu Val Gln
339 465 470 475 480
341 Asp Gly Ile Lys Val Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr
342 485 490 495
344 Glu Lys Met Pro Glu Ser Ile Lys Phe Ile Lys Gln Lys His Gly Ala
345 500 505 510
347 Ile Arg Trp Ser Gly Asp Phe Thr Gln Gly Pro Gln Ser Ala Lys Thr
348 515 520 525
350 Arg Phe Trp Lys Asn Val Arg Tyr His Met Pro Val Gln Arg Arg Ser

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/731,175

DATE: 12/14/2001

TIME: 16:07:36

Input Set : N:\Crf3\RULE60\09731175.txt

Output Set: N:\CRF3\12142001\I731175.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:656 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:672 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:688 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:704 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8